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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.							
REFERENCE 1 (bases 1 to 1894)							
AUTHORS Kaufmann,J. and Xin,H.							
TITLE Expression of ets-domain proteins in cancer							
JOURNAL Patent: WO 0070092-A 1 23-NOV-2000;							
Chiron Corporation (US)							
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DEFINITION cds.
ACCESSION AF071538

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VERSION AF071538.1 GI:4007417
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SOURCE Homo sapiens
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REFERENCE 1 (bases 1 to 1894)
AUTHORS Oettingen,P., Finger,E., Sun,Z., Akbarali,Y., Thumrongsak,U.,
Bolatz,J., Grall,F., Dube,A., Weiss,A., Brown,U., Quinn,G., Kas,K.,
Endress,G., Kunsch,C., and Libermann,T.A.
PDEF, a novel prostate epithelium-specific ets transcription
factor, interacts with the androgen receptor and activates
prostate-specific antigen gene expression
J. Biol. Chem. 275 (2), 1216-1225 (2000)
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JOURNAL 2 (bases 1 to 1894)
MEDLINE Libermann,T.A., Oettingen,P., Kunsch,C. and Finger,E.
REFERENCE Direct Submission
AUTHORS Submitted (10-JUN-1998) Medicine, Beth Israel Deaconess Medical
JOURNAL Center, 330 Brookline Ave., Boston, MA 02215, USA
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 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE
 1 (bases 1 to 3317)
 AUTHORS Kaufmann, J. and Xin, H.
 TITLE Expression of ets-domain proteins in cancer
 JOURNAL Patent: WO 0070092-A 12 23-NOV-2000;
 Chiron Corporation (US)
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ACCESSION AL157372
VERSION AL157372.18 GI:11493236
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens

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REFERENCE
AUTHORS Skuce, C.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
COMMENT
On Nov 30, 2000 this sequence version replaced g1:11342772.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated repeat sequence elements. Where the sequence is
ambiguous, there is an annotation using the 'unsure' feature key.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; SW: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/projects/C.elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr6
RP11-375E1 is from the library RPCI-11.2 constructed at the Roswell
Park Cancer Institute by the group of Pieter de Jong. For further
details see http://bacpac.med.buffalo.edu/
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sections only once, except for a 100 base overlap.
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BASE COUNT 35470 a 38887 c 38740 g 37563 t
ORIGIN
alignment_scores:
Quality: 144.00 Length: 144
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-126-945B-2_COPY-2_335 x AL157372/rev ..
Align seg 1/1 to reverse of: AL157372 from: 1 to: 150660
1 GlySerAlaSerProGlyLeuSerSerValSerProSerHisLeuLeu 17
129737 GGCAGCGCCAGCCCGGCTGTGAGCAGCGTATCCCGCACCACTCTGCT 129688
17 uProProAspThrValSerArgThrGlyLeuGluLysAlaAlaGlyA 34
129687 GCCCCCAACAGGTGTGCGGACAGGCTTGGAGAAAGCGGACAGCGGG 129638
34 LValGlyLeuGluArgArgAspTrpSerProSerProAlaThrPro 50
129637 CAGTGTCTGAGAGAGAGCGGAGCTGAGTCCACATGCCAGCCGACGCC 129588

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51 gi|ungllyleuSerAlaPheTyrlleuSerTyrlpheasPmetleuTyPr 67
|||||
129587 GAGCAGGCGCTTCGCGCTTACCTCTCTACTTGTGACATCTCTACC 129538
|||||
67 OGLuSpSerSerrTPAlaAlaLysAlaProGlyAlaSerSerrArgJug 84
|||||
129537 TGAGGACAGCAGCTGGGCGACCGCCCTGGGCGCAGCTGGGAGG 129488
|||||
84 lUPProGluGluProGluGluGlnCysProValIleAspSerrIlaIaPro 100
|||||
129487 AGCCACCTGAGAGAGCTGACAGATGCCGCTCATTTGACAGCCACCCCA 129438
|||||
101 AlaGlySerLeuAspLeuValProGlyGlyLeuThrLeuGluGluHisSe 117
|||||
129437 GCGGGCACCCTGAGACTTGCTGCCGCGGCTGACCTTGAGAGAGCAGCTC 129388
|||||
117 rLeuGluGluValGlnSerMetValIaGlyGluValLeuLysAspIleG 134
|||||
129387 GCTGGAGCAGGTGCTGATGCTGATGCTGAGCGAAGTCTCAAGACATCG 129338
|||||
134 lUThrAlaCysAlaLysLeuLysAlaThrAla 144
|||||
129337 AGACGGCTGCACAGCTGCTCAACATCACCCGA 129306
|||||
seq_name: gb_rol:AB019436

seq_documentation_block:
LOCUS AB019436 1704 bp mRNA ROD 20-JAN-2000
DEFINITION Mus musculus mRNA for Prostate specific transcription factor ets.
ACCESSION AB019436
VERSION AB019436.1 GI:4760536
KEYWORDS Prostate specific transcription factor ets; mpse.
SOURCE Mus musculus (strain:C57BL/6) Adult male Colon Epithelial cdna to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (sites)
Yamada, N., Tamai, Y., Miyamoto, H. and Nozaki, M.
Cloning and expression of the mouse Pse gene encoding a novel Ets
family member
Gene 241 (2), 267-274 (2000)
20137504
2 (bases 1 to 1704)
Nozaki, M.
Direct Submission
Submitted (02-NOV-1998) to the DBJ/EMBL/GenBank databases. Masami
Nozaki, Osaka University, Institute for Microbial Diseases, 3-1,
Yamadaoka, Suita, Osaka 565-0871, Japan
(E-mail:mozaki@biken.osaka-u.ac.jp, Tel:81-6-879-8338,
Fax:81-6-879-8339)
FEATURES
source
1..1704
Location/Qualifiers
1..1704
/organism="Mus musculus"
/strain="C57BL/6"
/db_xref="taxon:10090"
/cell_type="Epithelial"
/dev_stage="Adult"
/sex="male"
/tissue_type="Colon"
362..1339
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362..1339
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/codon_start=1
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/db_xref="GI:4760537"
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PSPATPQGLSAFLSYFNMYPDSSVVAAPARAGEDPEPEQCPTVDSQASGS
TLDSHLEOVOSNVGVLKDIETACKLNTAPGDMSPGNVOKMLMTTEHOYRLRP
AGKAFOELGKELCAMSEDEPRORAPLGGDVLHMHLDIKMSAMMKERTSCTLHYCA

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polya_site
BASE COUNT 369 a 527 c 491 g 317 t
ORIGIN
1704
SMESEGTDEVDSSCSGPIILMOFLKELLKPSYGRFIRMLNKEGIERIEDSAQ
VARLMGVRNRNRPMAMNDKLSRSIRQYRKGIIRKPDISORLYOFVHPV"
/Note="10 a nucleotides"

alignment_scores:
Quality: 54.00 Length: 54
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
us-09-126-945b-2_copy_2_335 x AB019436 ..

Align seg 1/1 to: AB019436 from: 1 to: 1704

238 GLUValAspSerSerCysSerGlyGlnProIleHisLeuTyPrGlnPheLe 254
|||||
1046 GAGGTGAGCTGCTGCTGCTCGGCGACCCATTCACCTGTGGCAGTTCTT 1095
|||||
254 ULysGluLeuLeuLeuLysProHisSerTyrglyArgPheIleArgTyPrL 271
|||||
1096 GAAAGAACTGCTGCTCAAGCCACACACTATGGCGGCTTCATCGCTGGC 1145
|||||
271 euAsnLysGluLysGlyIlePheLysIleGluAspSerAlaGlnValAla 287
|||||
1146 TCACACAGAGAGAAAGCATCTTCAAAATTGAGACATCAGCAGAGTGCC 1195
|||||
288 ArgLeuTyPrGly 291
|||||
1196 CGACTGTGGGGT 1207
|||||

seq_name: gb_in3:DR02TS4A

seq_documentation_block:
LOCUS DR02TS4A 362 bp DNA INV 28-SEP-1999
DEFINITION Drosophila melanogaster chromosome 3 D-ets-4 DNA binding domain
protein gene, partial cds.
ACCESSION M88474
VERSION M88474.1 GI:157195
KEYWORDS
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 362)
Chen, T., Bunting, M., Karim, F.D. and Thummel, C.S.
Isolation and characterization of five Drosophila genes that encode
an ets-related DNA binding domain
Dev. Biol. 151, 176-191 (1992)
92249640
FEATURES
source
1..362
Location/Qualifiers
1..362
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/product="D-ets-4 DNA binding domain protein"
<1..345
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/translation="TNASNGTATVVRKNGRGTGGGSHILMQLFKELLASPOVNGT
AIRWIDSKGIFKIEDSVRAKLGRKRKRPANMYDKLSINQYKKGIMKKTBSQ
RLVYQFCHPYSQ"
BASE COUNT 90 a 99 c 113 g 60 t
ORIGIN

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This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive web site (<http://www.fruitfly.org/sequence/>) or send email to bdg@fruitfly.berkeley.edu.

FEATURES

SOURCE

1. 193245
/organism="Drosophila melanogaster"
/strain="y; cn bw sp"
/db_xref="taxon:7227"
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/clone="BACR10J03 (D786)"
/clone_id="Rpci-98 (Roswell Park Cancer Institute Drosophila melanogaster BAC library, partial EcorI in pBAC3.6)"

BASE COUNT 55736 a 43163 c 42757 g 51589 t
ORIGIN

alignment_scores:
Quality: 24.00 Length: 24
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-126-945b-2_copy-2_335 x AC008217 ..

Align seq 1/1 to: AC008217 from: 1 to: 193245

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56236 CGCAGAACCCACCGCGCATGATGATAGTGTCCCGCTCCATCAG 56285

309 gGlnTyTfTyfLybLyGlyIle 316

56286 GCAGTACTACAAAGGAGATC 56307

seq_name: gb_in2:AE003762

seq_documentation_block:

LOCUS AE003762 230940 bp DNA INV 05-OCT-2000
DEFINITION Drosophila melanogaster genomic scaffold 142000013386035 section 87
of 105, complete sequence.

ACCESSION AE003762 AE002708
VERSION AE003762.2 GI:10726810

KEYWORDS

SOURCE

ORGANISM

fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 230940)

REFERENCE

AUTHORS

Adams,M.D., Celniker,S.E., Holt,R.A., Evans,C.A., Gocayne,J.D.,
Amanatides,P.G., Scherer,S.E., Li,P.W., Hoskins,R.A., Galle,R.F.,
Georgie,R.A., Lewis,S.E., Richards,S., Ashburner,M., Henderson,S.N.,
Sutton,G.G., Wortman,J.R., Yandell,M.D., Zhang,Q., Chen,L.X.,
Brandon,R.C., Rogers,Y.H., Blazek,R.G., Champe,M., Pfeiffer,B.D.,
Man,R.H., Doyle,C., Baxter,E.G., Helt,G., Nelson,C.R., Gabor
Miklos,G.L., Adril,J.F., Agbayani,A., An,H.J.,
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Bencos,P.V., Bereman,B.P., Bhandari,D., Bonsharkov,S., Botkova,D.,
Botchan,M.R., Bouck,J., Brokstein,P., Brottler,P., Burtis,K.C.,
Bushman,D.A., Butler,H., Cadieu,E., Center,A., Chandra,I.,
Cherry,J.M., Cawley,S., Dahlke,C., Davenport,L.B., Davies,P., de
Pablo,B., Delcher,A., Deng,Z., Mays,A.D., Dew,I., Dietz,S.M.,
Dunn,P., Durbin,K.J., Evans,J., Gabor,M., Dugan-Rocha,S., Dunkov,B.C.,
Fleischmann,M., Foster,C., Gabriellian,A.E., Garg,N.S.,
Gibbs,R.A., Glaser,K., Glodek,A., Gong,F., Gorrell,J.H., Gu,Z.,
Guan,P., Harris,M., Harris,N.L., Harvey,D., Helman,T.J.,

TITLE
JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
SOURCE

Hernandez,J.R., Houck,J., Hostin,D., Houston,K.A., Howland,T.J.,
Wei,M.H., Ibegwam,C., Jallali,M., Kalush,F., Karpn,G.H., Ke,Z.,
Kernison,J.A., Ketchum,K.A., Kimmel,B.E., Kodira,C.D., Kraft,C.,
Krautiz,S., Kulp,D., Lai,Z., Lasako,P., Lei,Y., Levitsky,A.A.,
Li,J., Li,Z., Liang,Y., Lin,X., Liu,X., Matel,B., McIntosh,T.C.,
Meloed,M.P., McPherson,D., Merkulov,G., Mlshna,N.V., Mobarry,C.,
Morris,J., Moshrefi,A., Mount,S.M., Moy,M., Murphy,B., Murphy,L.,
Muzny,D.M., Nelson,D.L., Nelson,D.R., Nelson,K.A., Nixon,K.,
Nusskern,D.R., Pacle,J.M., Palazolo,M., Pltman,G.S., Pan,S.,
Pollard,J., Puri,V., Reese,M.G., Reinert,K., Remington,K.,
Saunders,R.D., Scheeler,F., Shen,H., Shue,B.C., Siden-Klamos,I.,
Stimpson,M., Skupski,M.P., Smith,T., Spier,E., Spradling,A.C.,
Stapleton,M., Strong,R., Sun,E., Sytkas,R., Tector,C., Turner,R.,
Venter,E., Wang,A.H., Wang,X., Wang,Z.T., Wasserman,D.A.,
Weinstock,G.M., Weissbach,J., Williams,S.M., Woodage,T.,
Worley,K.C., Wu,D., Yang,S., Yao,Q.A., Ye,J., Yeh,R.F.,
Zaveri,J.S., Zhan,M., Zhang,G., Zhao,Q., Zheng,L., Zheng,X.H.,
Zhong,F.N., Zhong,W., Zhou,X., Zhu,S., Zhu,X., Smith,H.O.,
Gibbs,R.A., Myers,E.W., Rubin,G.M. and Venter,J.C.
The genome sequence of Drosophila melanogaster
Science 287 (3461), 2185-2195 (2000)
2 (bases 1 to 230940)
Adams,M.D., Celniker,S.E., Gibbs,R.A., Rubin,G.M. and Venter,C.J.
Direct Submission
Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
On Oct 9, 2000 this sequence version replaced gi:7301615.
Location/Qualifiers
1. 230940
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/chromosome="3R"
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7946..8563,8624..9356,9414..9551,9612..9910,9967..10145,
10199..10805,10863..11420,11477..11780,11842..12791,
12847..14304,14685..14853,14914..15248,15346..15579,
15636..15869)
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/db_xref="FLYBASE:FBgn0039536"
/evidence="not_experimental"
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/evidence="not_experimental"
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/evidence="not_experimental"
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/translation="MNGSAQPAVARHLICVLPFOLATMTYNAAGTAAGCATSNTN
NNNLTNNNSHGANNNDPDDPSGLDGLGIPVSOTFLMRO IAPFIRPKGLHE
STLSEAEAKSPFEKLVYQNIQFGLSPRLKGLGVIFRMLRLLGAL IAPVHAKCALIE
NRKMDAIGPVERKLVYQNIQFGLSPRLKGLGVIFRMLRLLGAL IAPVHAKCALIE
SVPTIVSLVCICCTYTPPKGIGFPLSGEWH"
16549..18002
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CDS
134..1225
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/product="Ers4 transcription factor"
/protein_id="AADI942.1"
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/translational="MSTGEVCSVPTPMNDPAIHLAEISMGSTLLDILIQOQORN
GSPSPFGSGFLPSPDMGSPFPQNGFPPTQMGSTIQOQGNISLEENEMRL
LREMIPTDLEDCIKLNLINNYCTPEDVQKMLCIVNRFELGEMGHFTINGFTL
ATLDVDFNRHRAKCGDILYSVCLKSSIHEDVAQVVAQGMNPIQPSHFTTG
APTTMPPKTYTPVSPVATPDGSGSGSPSDEISIPSPAPSPNTSMTPNHG
IDLMQFLKELLQPNISYCIKRIWDTGCIKFIEDSEVAVRLGLKRNPRAMNYDL
RSIRQYRKGIKMKTEVSQRLVYQFVTPC"

BASE COUNT      528 a      448 c      379 g      477 t
ORIGIN

alignment_scores:
Quality: 20.00      Length: 20
Ratio: 1.000      Gaps: 0
Percent Similarity: 100.000      Percent Identity: 100.000

alignment_block:
US-09-126-945B-2_COPY_2_335 x AF106964 ..
Align seg 1/1 to: AF106964 from: 1 to: 1832

293 ArglybAnaATProAlaMetAsnTyTrAspLyLeuSerArgSerIleAr 309
|||||
1097 AGGAAAGACAGCGCGCATGACACGACGACGCTCTCCCTCCATCAG 1146
309 GGLTYCTYr 312
|||||
1147 GCAGTACTAC 1156
seq_name: gb_pr9:HSERM12

seq_documentation_block:
LOCUS HSERM12 163 bp DNA PRI 25-SEP-1996
DEFINITION H.sapiens erm gene, exon 12.
ACCESSION X96376
VERSION X96376.1 GI:1418779
KEYWORDS erm gene; transcription factor.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 163)
Monte,D., Coutte,L., Deville,F., Defosse,P.A., Le Contat,M.,
Stehlin,D., Berger,R. and de Launoit,Y.
Genomic organization of the human ERM (ETV5) gene, a PEA3 group
member of ETS transcription factors
Genomics 35 (1), 236-240 (1996)
JOURNAL
MEDLINE
2 (bases 1 to 163)
De Launoit,Y.P
Direct Submission
Submitted (02-FEB-1996) Y.P. De Launoit, CNRS URA 1160 - Inst.
Pasteur de Lille, 1 rue Calmette, F- 59019 Lille Cedex, FRANCE
COMMENT
See X76184 for mRNA sequence of erm gene.
FEATURES
location/Qualifiers
1..163
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/db_xref="taxon:9606"
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33..134
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33..134
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/function="transcription factor"

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ORIGIN

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Quality: 14.00      Length: 14
Ratio: 1.000      Gaps: 0
Percent Similarity: 100.000      Percent Identity: 100.000

alignment_block:
US-09-126-945B-2_COPY_2_335 x HSERM12 ..
Align seg 1/1 to: HSERM12 from: 1 to: 163

294 LysAsnArgProAlaMetAsnTyTrAspLyLeuSerArgSer 307
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57 AAGAACCGCGCCGCGCATGACATGACACGACGACGCTCT 98
seq_name: gb_pat2:E06024

seq_documentation_block:
LOCUS E06024 473 bp RNA PAT 29-SEP-1997
DEFINITION cDNA encoding a protein(E1A-F) which binds to enhancer core region
of adenovirus E1A gene.
ACCESSION E06024
VERSION E06024.1 GI:2174211
KEYWORDS JP 1993328975-A/1.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 473)
Tono,F., Yoshida,K. and Fujinaga,M.
E1A-F GENE
Patent: JP 1993328975-A 1 14-DEC-1993;
TAKARA SHUZO CO LTD
OS Homo sapiens (human)
PN JP 1993328975-A/1
PD 14-DEC-1993
PI 02-JUN-1992 JP 1992165453
PT TONO FUMIHIRO, YOSHIDA KOICHI, FUJINAGA MEGUMI PC C12N15/34;
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: cell_line=HeLa cells;
CC *source: clone=lamda3-16;
FH key Location/Qualifiers
FH CDS 1..468
FT 1..468
FT /product="protein(E1A-F) which binds to FT
FT enhancer core
FT region of adenovirus E1A gene' FT 3'UTR
FT 469..473.
FT Location/Qualifiers
1..473
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ORIGIN

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Quality: 14.00      Length: 14
Ratio: 1.000      Gaps: 0
Percent Similarity: 100.000      Percent Identity: 100.000

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Align seg 1/1 to: E06024 from: 1 to: 473

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166 AAGAACCGCGCCGCGCATGATTAACGACAAAGCTGAGCCGCTCG 207
